

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 1, 2005, 13:15:28 ; Search time 35 Seconds

(without alignments)
3183.400 Million cell updates/sec

Title: US-10-659-782A-11

Perfect score: 1030

Sequence: 1 actctggtggtgctgtt.....tggcagcagaggggtgggg 579

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2.1/USPTO_spool_p/US10659782/runat_01022005_130352_14264/app_query.fasta_1.775
-DB=PIR_79 -QFMT=fastan -SUFFIX=xpr -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=BITS -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODES=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10659782 @CEN 1 1.63 @runat_01022005_130352_14264 -NCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 326 | 31.7 | 117 | 1 A59316 | ghrelin precursor |
| 2 | 256 | 24.9 | 117 | 1 B59316 | ghrelin precursor |
| 3 | 112 | 10.9 | 1344 | 1 A35175 | mucin 1 precursor |
| 4 | 105 | 9.8 | 152 | 2 T34649 | hypothetical prote |
| 5 | 103.5 | 10.0 | 379 | 2 T05441 | proline-rich prote |
| 6 | 103.5 | 10.0 | 379 | 2 D85257 | extensin-like prot |
| 7 | 100 | 9.7 | 620 | 2 S06733 | hydroxyproline-ric |
| 8 | 99.5 | 9.7 | 317 | 2 A28996 | proline-rich prote |
| 9 | 99.5 | 9.7 | 381 | 2 S16506 | hypothetical prote |
| 10 | 99 | 9.6 | 383 | 2 S32975 | gene BCRF2 protein |
| 11 | 98.5 | 9.6 | 349 | 2 T05857 | hypothetical prote |
| 12 | 98.5 | 9.2 | 356 | 1 WJHU2H | homeotic protein H |
| 13 | 98 | 9.5 | 347 | 2 S10571 | mucin 1 precursor, |
| 14 | 96.5 | 9.4 | 506 | 2 B56201 | transcription fact |

| | | | | | | |
|----|------|-----|------|---|--------|---------------------|
| 15 | 96.5 | 9.4 | 514 | 2 | A56201 | transcription fact |
| 16 | 96 | 9.3 | 839 | 2 | F75518 | hypothetical prote |
| 17 | 95 | 9.2 | 632 | 2 | T00084 | hypothetical prote |
| 18 | 94.5 | 9.2 | 1690 | 1 | CGHUIB | collagen alpha 4(I |
| 19 | 94 | 8.8 | 1216 | 2 | T34101 | hypothetical prote |
| 20 | 94 | 9.1 | 3164 | 1 | WMBEH6 | UL16 protein - hum |
| 21 | 93.5 | 9.1 | 349 | 2 | JCS881 | myocyte enhancer f |
| 22 | 93.5 | 9.1 | 672 | 2 | I40333 | tracheal colonizat |
| 23 | 93 | 9.0 | 1575 | 2 | S68448 | synaptotjanin, 170K |
| 24 | 92.5 | 8.7 | 454 | 2 | T35380 | probable membrane |
| 25 | 92.5 | 8.7 | 591 | 2 | E83039 | probable thiol-dis |
| 26 | 92 | 8.7 | 135 | 2 | S12549 | hypothetical prote |
| 27 | 92 | 8.9 | 374 | 2 | A42270 | alpha (1,3) fucosy |
| 28 | 92 | 8.9 | 544 | 2 | S15664 | transcription fact |
| 29 | 91.5 | 8.9 | 511 | 1 | A48560 | UL54 protein - hum |
| 30 | 91.5 | 8.9 | 512 | 1 | WMBEY4 | UL54 protein - hum |
| 31 | 91.5 | 8.9 | 729 | 2 | E70803 | hypothetical prote |
| 32 | 91.5 | 8.9 | 1006 | 2 | T42731 | atrophin-1 related |
| 33 | 91.5 | 8.9 | 1091 | 2 | S33596 | protein-tyrosine k |
| 34 | 91.5 | 8.6 | 1232 | 2 | I38496 | anion exchanger 3 |
| 35 | 91 | 8.8 | 240 | 2 | A24264 | proline-rich prote |
| 36 | 91 | 8.8 | 539 | 2 | T28770 | hypothetical prote |
| 37 | 91 | 8.8 | 576 | 2 | T36729 | probable serine/th |
| 38 | 91 | 8.8 | 901 | 2 | A49227 | sialidase - Actino |
| 39 | 90.5 | 8.8 | 339 | 2 | JCS882 | myocyte enhancer f |
| 40 | 90.5 | 8.5 | 468 | 2 | S26741 | T-cell glycoprotei |
| 41 | 90.5 | 8.8 | 587 | 2 | T41653 | probable transcrip |
| 42 | 90 | 8.4 | 431 | 2 | S09824 | hypothetical prote |
| 43 | 90 | 8.7 | 1184 | 2 | G01763 | atrophin-1 - human |
| 44 | 90 | 8.7 | 1734 | 2 | A54602 | microtubule-associ |
| 45 | 90 | 8.7 | 1794 | 2 | T38459 | hypothetical diver |

ALIGNMENTS

RESULT 1

A59316
ghrelin precursor - human
N:Alternate names: preproghrelin
C:Species: Homo sapiens (man)
C:Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: A59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-117 <KOU>
A:Cross-references: UNIPROT:Q9UBU3; GB:AB029434; NID:g6691571; PIDN:BAA89371.1; PID:g6691571
A:Experimental source: tissue stomach endocrine cells
A:Note: submitted to GenBank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth hormone) from the anterior pituitary gland.
C:Superfamily: motilin
C:Keywords: hormone; lipoprotein; stomach
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <MAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Alignment Scores:

Pred. No.: 8.21e-21 Length: 117
Score: 326.00 Matches: 74
Percent Similarity: 53.19% Conservative: 1
Best Local Similarity: 52.48% Mismatches: 0
Query Match: 31.65% Indels: 66
DB: 1 Gaps: 1

US-10-659-782A-11 (1-579) x A59316 (1-117)

QY 112 ATGCCCTCCAGGACCGTCTGGAGCTCTGCTCGGCATGCTCTGGCTGACTG 171
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Db      1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY      172 GCCATGGCAGGCTCCAGCTTCTCTGAGCCCTGAACACACAGAGAGTCCAGGTGAGACCTCCC 231
Db      21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY      232 CACAAAGCCCAATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 291
Db      37 ----- 37
QY      292 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCTCCAGAGACAAAGGACTCTGGGTCTGAC 351
Db      37 ----- 37
QY      352 CTCACGTGTTTCTGGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCCCTTCC 411
Db      37 ----- 37
QY      412 AGCAGAGAAAGAGTGGAAAGCCACAGCAAGCTGCAGCCCGAGCTTACAGGCT 471
Db      38 -----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAlaLeuAlaGlyT 56
QY      472 GGTCTCGCCCGGAGATGAGTCAAGCAGAGGGGAGAGGATCAACTGGAACTCCGG 530
Db      56 rpleuArgProGluAspGlyGlyGlnAlaGluGlyAlaGluAspGluLeuGluValArg 75

RESULT 2
B59316
ghrelin precursor - rat
N;Alternate names: preproghrelin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jun-2000 #sequence revision 16-Jun-2000 #text_change 09-Jul-2004
C;Accession: B59316
R;Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A;Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A;Reference number: A59316; MUID:20067959; PMID:10604470
A;Accession: B59316
A;Status: not compared with conceptual translation
A;Molecule type: mRNA; protein
A;Residues: 1-117 <KOJ>
A;Cross-references: UNIPROT:Q9QYH7; GB:AB029433; NID:96691569; PIDN:BAA89370.1; PID:9669
A;Experimental source: strain SD; tissue stomach endocrine cells
A;Note: submitted to GenBank, June 1999
C;Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth hormone) from the hypothalamus.
C;Superfamily: motilin
C;Keywords: hormone; lipoprotein; stomach
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-51/Product: ghrelin #status predicted <MAT>
F;52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;26/Binding site: octanoate (Ser) (covalent) #status experimental

Alignment Scores:
Pred. No.: 1.27e-14 Length: 117
Score: 256.00 Matches: 60
Percent Similarity: 46.81% Conservative: 6
Best Local Similarity: 42.55% Mismatches: 9
Query Match: 24.85% Indels: 66
Db: 1 Gaps: 1

US-10-659-782A-11 (1-579) x B59316 (1-117)
QY      112 ATGCCCTCCCGAGGACCGTCTCGAGCTCTCTGCTGGCATGCTCTGGCTGGAGCTTG 171
Db      1 MetValSerSerAlaThrIleCysSerLeuLeuLeuLeuSerMetLeuTrpMetAspMet 20
QY      172 GCCATGGCAGGCTCCAGCTTCTCTGAGCCCTGAACACACAGAGAGTCCAGGTGAGACCTCCC 231
Db      21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnLys--Ala----- 35
QY      232 CACAAAGCCCAATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 291
Db      35 ----- 35

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QY      292 CAGCAGCGCCATCTCTGGGCTTCTAGTCTTCTCCAGAGACAAAGGACTCTGGGTCTGAC 351
Db      35 ----- 35
QY      352 CTCACGTGTTTCTGGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCCCTTCC 411
Db      36 -----G 36
QY      412 AGCAGAGAAAGAGTGGAAAGCCACAGCAAGCTGCAGCCCGAGCTTACAGGCT 471
Db      36 lnglnArgLysGluSerLysLysProProAlaLysLeuGlnProArgAlaLeuGluGlyT 56
QY      472 GGTCTCGCCCGGAGATGAGTCAAGCAGAGGGGAGAGGATGAAGTGAAGTCCGG 530
Db      56 rpleuHisProGluAspArgglyGlnAlaGluGlyAlaGluGluLeuGluLeuArg 75

RESULT 3
A35175
mucin 1 precursor, repetitive splice form A [validated] - human
N;Alternate names: breast carcinoma-associated DF3 antigen; core protein KP39; episialin
N;Contains: mucin 1 precursor, epithelial tumor antigen splice form; mucin 1 precursor,
C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text_change 02-Jun-2000
C;Accession: A35175; A35175; A35886; A35887; S10572; S40293; A36735; PX0066; S10218; S51
R;Ligtenberg, M.J.L.; Vos, H.L.; Gennissen, A.M.C.; Hilkens, J.
J. Biol. Chem. 265, 5573-5578, 1990
A;Title: Episialin, a carcinoma-associated mucin, is generated by a polymorphic gene enc
A;Reference number: A35175; MUID:90202794; PMID:2318625
A;Accession: A35175
A;Molecule type: mRNA
A;Residues: 1-952,1033-1344 <LIG>
A;Cross-references: GB:M32738; GB:J05288; NID:g182121; PIDN:AAA35804.1; PID:g182124; GB:
A;Experimental source: splice form A
A;Note: GenBank entries HUMEPISIA1 and HUMEPISIA2 present only the amino-and carboxyl-en
A;Accession: B35175
A;Molecule type: mRNA
A;Residues: 1-19,29-952,1033-1344 <LIG2>
A;Cross-references: GB:M32739; GB:J05288; NID:g182126; PIDN:AAA35806.1; PID:g182129; GB:
A;Experimental source: splice form B
A;Note: GenBank entries HUMEPISIB1 and HUMEPISIB2 present only the amino-and carboxyl-en
R;Gendler, S.J.; Lancaster, C.A.; Taylor-Papadimitriou, J.; Duhig, T.; Peat, N.; Burchel
J. Biol. Chem. 265, 15286-15293, 1990
A;Title: Molecular cloning and expression of human tumor-associated polymorphic epitheli
A;Reference number: A35886; MUID:90368715; PMID:1697589
A;Accession: A35886
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-19,29-952,1033-1344 <GEN>
A;Cross-references: GB:J05581; NID:g188869; PIDN:AAA59876.1; PID:g188870
A;Note: GenBank entry HUMMUCAB includes one copy of the tandemly repeated sequence
R;Lan, M.S.; Batra, S.K.; Qi, W.N.; Metzgar, R.S.; Hollingsworth, M.A.
J. Biol. Chem. 265, 15294-15299, 1990
A;Title: Cloning and sequencing of a human pancreatic tumor mucin cDNA.
A;Reference number: A35887; MUID:90368716; PMID:2394722
A;Accession: A35887
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A;Cross-references: GB:J05582; NID:g189598; PIDN:AAA60019.1; PID:g189599
A;Note: GenBank entry HUMPMUUCAB contains four fewer copies of the tandemly repeated sequ
R;Wreschner, D.H.; Hareuveni, M.; Tsarfaty, I.; Smorodinsky, N.; Horev, J.; Zaretsky, J.
Eur. J. Biochem. 189, 463-473, 1990
A;Title: Human epithelial tumor antigen cDNA sequences. Differential splicing may genera
A;Reference number: S10571; MUID:90276413; PMID:2351132
A;Accession: S10572
A;Molecule type: mRNA
A;Residues: 1-19,29-155,'P',157-175,'P',177-182,'A',184-212,1033-1344 <WRE>
A;Cross-references: EMBL:X52229; NID:g37053
R;Wreschner, D.H.
submitted to the EMBL Data Library, March 1990
A;Reference number: S40293

```

Db 153 -ThrArgProAlaProGlySerThrAlaProProAlaHisGlyValThrSerAlaProAs 172

Qy 263 CACTTAGCAACACCACTCTGTGACCTGCAGCAGCAGCCCAATC-----TCTGGGCTTCAGTC 318

Db 172 pThr--ArgProAla-----ProGlySerThrAlaProProAlaHisGlyValThrSe 189

Qy 319 TTCTCCAGAGCAACAAGGACTCTGGGTCTGACCTCACTCTGTTCTTGGAAGACATGGGGG 378

Db 189 rAlaProAspThrArgProAlaProGlySerThrAla-----ProProAlaHis--Gl 206

Qy 379 CTTAGAGCTCCTAAACACACTGTTTCCCCCTTCCAGCAGAG-----AAAGG 423

Db 206 yValThrSerAlaProAspThrArgProAlaProGlySerThrAlaProProAlaHisGl 226

Qy 424 AGTCGAAGAAGCCACCAGCAAGCTGCAGGCCCGCAGCTCTAGCAGGCTGGCTCCGCCCGG 483

Db 226 yValThrSerAlaProAspThrArgProAlaProGlySerThr-----AlaProProAl 244

Qy 484 AAGATGGAGTCAAGC-----AGAAGGGCAGAGAGTGAAGTGAAGTCCCGG 531

Db 244 aHisGlyValThrSerAlaProAspThrArgProAlaProGlySerThrAlaProProAl 264

Qy 532 TCGGTACTCTGCAGT 547

Db 264 aHisGlyValThrSer 269

RESULT 4

T34649

hypothetical protein SC1A11.02c SC1A11.02c - Streptomyces coelicolor (fragment)

C/Species: Streptomyces coelicolor

C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999

C/Accession: T34649

R/Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandram, submitted to the EMBL Data Library, January 1999

A/Reference number: Z21551

A/Accession: T34649

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-152 <SEE>

A/Cross-references: EMBL:AL035205; PIDN:CAA22742.1; GSPDB:GN0070; SCODEB:SC1A11

A/Experimental source: strain A3(2)

C/Genetics:

A/Gene: SCODEB:SC1A11.02c

Alignment Scores:

| | | | |
|------------------------|--------|---------------|-----|
| Pred. No.: | 0.288 | Length: | 152 |
| Score: | 105.00 | Matches: | 42 |
| Percent Similarity: | 41.60% | Conservative: | 10 |
| Best Local Similarity: | 33.60% | Mismatches: | 41 |
| Query Watch: | 9.84% | Indels: | 32 |
| DB: | 2 | Gaps: | 6 |

US-10-659-782A-11 (1-579) x T34649 (1-152)

Qy 372 TGTCCTTCAGAAACATGATAGGTCCAGACCAGAGATCCTTTGTGCTCTGGAGAGACTGA 313

Db 1 CysProAla---SerSerProAlProProArg-----SerSerGly 13

Qy 312 AGCCACAGATGGCGCTGCTGCTCCAGTCCAGTCCAGAGCTGGTTGCTAAGTGCAGG----- 258

Db 14 ThrPro-ArgGlyAlaCysCysSerSerSerArgThrThrAlaArgGlyGlyArgCysPr 33

Qy 257 -----GCTGAAACAACATGTGGGGCTTTGGGGAGGCTCTCAC 220

Db 33 oAlaGlyArgSerSerProGlyThrGlyArgAlaArgGlyArgAlaArgGlyGlyArgPr 53

Qy 219 CTGG-----ACTCTCTGGTGTTCAGGCTCAGGAAGCTGGAG----- 182

Db 53 oTrpArgArgSerAspSerThr-CysGlySerAlaGlyCysSerArgTrpThrGlyArgT 73

Qy 181 -----CTGCCATGGCCAAAGTCCAGCAGATGTCGCCAGGAGCAGGAGCTGCACAGCGT 127

Db 73 hrGlyArgAlaGlyProArgSerTrpArgThrCysThrThrAlaGlyCysCysArgArgT 93

Db 172 uSerProProLeuValGlyIleCysSerLysAsnAspThrGluLeuLysIleCysAlaG1 192
QY 470 CTGGCTCCCGCGAGATGGA-----GGTCAAGCAGAGAGGGCGAGAGATGA 517
Db 192 yLeuLeuAlaIleSerAspGlyLeuLeuThrThrGlyArgAlaGluProCysCysSerI1 212
QY 518 ACTGGAAGTCCGGTGGTGTACCTCTGACGTTTATGCTTCTCTGGGAGC 566
Db 212 eileArgAnValSerAspLeuAspAlaValThrCysPheCysLysSer 228
RESULT 7
S06733
hydroxyproline-rich glycoprotein precursor - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S06733
R:Keller, B.; Lamb, C.J.
Genes Dev. 3, 1639-1646, 1989
A:Title: Specific expression of a novel cell wall hydroxyproline-rich glycoprotein gene
A:Reference number: S06733; MUID:90128263; PMID:2612909
A:Accession: S06733
A:Molecule type: DNA
A:Residues: 1-620 <KEL>
A:Cross-references: UNIPROT:PI3983; EMBL:X13885; NID:g19866; PIDN:CAA32090.1; PID:g19867
C:Superfamily: hydroxyproline-rich glycoprotein
C:Keywords: glycoprotein
Alignment Scores:
Pred. No.: 0.795 Length: 620
Score: 100.00 Matches: 52
Percent Similarity: 37.04% Conservative: 8
Best Local Similarity: 32.10% Mismatches: 72
Query Match: 9.71% Indels: 30
DB: 2 Gaps: 10
US-10-659-782A-11 (1-579) x S06733 (1-620)
QY 30 CCGTCTCTATATAGACTGACAGCAGGACCA-----CTCGCCGAG 74
Db 35 ProProProVal-----ThrSerGlnProProProSerSerIleGlyLeuSerPro 51
QY 75 GACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCGCTCCCTCCAGGAGACCGTCTG 134
Db 52 ProSerAlaProThrThrThrProProSerArgGlyHis---ValProSerProArgHis 70
QY 135 CAGCCTCTGCTCTGGCATGCTCTGGCTGGACTTGGCCACTGGCAGGCTCCAGCTT--- 191
Db 71 AlaPro-----ProArgHisAlaTyrProProProSerHisGlyHisLeuProProSer 88
QY 192 -----CCTGAGGCC-----TGAACACAGAGAGTCCAGGTGAGACCTCCCA 233
Db 89 ValGlyGlyProProProHisArgGlyHisLeuProProSerArgGlyPheAsnProPro 108
QY 234 CAAAGCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGAGCA 293
Db 109 ProSerProValle-----SerProSerHisProProProSerTyr-----GlyAla 124
QY 294 GCAGCGCCATCTCTGGGCTTCACTCTTCTCCAGAGACAAAGGACTCTGGGTCTGACCT 353
Db 125 ProProProSerHisGlyProGlyHisLeuProProSerHisGlyGlnArgProProSerPro 144
QY 354 ----CACTGTTCTGGAGACATGGGGCTTAGTCTTAACAGACTTTTCCCTTC 410
Db 145 SerHisGlyHisAlaProProSerGlyHisThrProProArgGlyGlnHisProPro 164
QY 411 CAGCAGAGAAAGAGTGC-----AAGAAGCCACAGCCAGGCTG 449
Db 165 SerHisArgGlyProProProProSerProProSerArgHisGlyHisProProProThrTyrAla 184
QY 450 CAGCCC 455
Db 185 GlnPro 186

RESULT 8
A28996
proline-rich protein M14 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A28996
R:Ann, D.K.; Smith, K.; Carlson, D.M.
J. Biol. Chem. 263, 10887-10893, 1988
A:Title: Molecular evolution of the mouse proline-rich protein multigene family. Insert
A:Reference number: A28996; MUID:88273214; PMID:2839509
A:Accession: A28996
A:Molecule type: DNA
A:Residues: 1-317 <ANN>
A:Cross-references: UNIPROT:Q62103; GB:M23236; GB:J03891; NID:g200535; PIDN:AAAS3048.1
C:Genetics:
A:Introns: 22/1
C:Superfamily: proline-rich protein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-317/Product: proline-rich protein M14 #status predicted <MAT>
Alignment Scores:
Pred. No.: 0.882 Length: 317
Score: 99.50 Matches: 47
Percent Similarity: 33.33% Conservative: 4
Best Local Similarity: 30.72% Mismatches: 70
Query Match: 9.66% Indels: 32
DB: 2 Gaps: 6
US-10-659-782A-11 (1-579) x A28996 (1-317)
QY 44 AGACCTGACAGCAGGACCACTCCGCGAGGACTGCAGGCCACCTGTCTGCAACCCAG 103
Db 103 ArgProProGln---GlyProProProGly-----Gly 113
QY 104 CTGAGCGCATGCCCTCCCGAGGACGCTGCAGCCT-----CCTGCTCTCTCGGCATGC 157
Db 114 ProGlnProArgProProGlnGlyProPro-ProProGlyGlyProGlnProArgProPr 133
QY 158 TCTGGCTGGACTTGGCCATGCGAGGCTCCAGCTTCTGAGCCCTGAACACAGAGAGTCC 217
Db 133 oGlnGlyProProProProGlyGlyProGlnGlnArgProProGlnGlyProProPr 153
QY 218 AGGTGAGACTCCCAAGAGCCACATGTTGTCAGCCCTGCGCACTAGCAACACAGC 277
Db 153 oGlyGlyProGlnProArgProProGlnGlyProProProProAlaGlyProGlnProAr 173
QY 278 TCTGTGACTGGAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGG 337
Db 173 gPro---ProGlnGlyProProProProAlaGlyProHisLeuArgProThrGln----- 190
QY 338 ACTCTGGGTCTGACCTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAAACAGAC 397
Db 191 -----GlyProProProTh 195
QY 398 TGTTCCTCCCTTCCAGCAGAGAAAGAGTGCAGAGCCAGCCAGCCAGCTCAGCCCG 457
Db 195 rGlyGlyProGlnGlnArgTyrProGlnSerProProProGlyGlyProGlnProAr 215
QY 458 AGCTCTAGCAGGCTGGCTCCGCGCGAGAGATGAGGT 494
Db 215 gProProGlnGly-----ProProProProGlyGly 225
RESULT 9
S16506
hypothetical protein - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Nov-1994
C:Accession: S16506
R:Mariman, E.C.M.; Schepens, J.T.G.; Wieringa, B.
Nucleic Acids Res. 17, 6385, 1989
A:Title: Complete nucleotide sequence of the human creatine kinase B gene.
A:Reference number: S15935; MUID:89366665; PMID:2771648

Best Local Similarity: 30.00% Mismatches: 52
Query Match: 9.37% Indels: 37
DB: 2 Gaps: 10

US-10-659-782A-11 (1-579) x B56201 (1-506)

```
QY 62 ACCACTCCGCCAGGACTGCAG--GCCACCTGTCTGCAACCCAGCTGAGGCGCATGCCCT 118
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 343 SerSerProAlaGlyLeuAlaLeuGlyAsnValThrAlaTrpGln---GlnProGlnPro 361
QY 119 CCCAGGACCGTCTGTCAGCCCTCTGCTCCCTGGCATGCTCTGGCTGGAGATTGGCCATGG 178
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 362 ProGlnProGln-ProProGlnProProGln----- 372
QY 179 CAGGCTCCAGCTTCTTCAGCCCTGACACACAGAGAGCTCAGGTGAGACCTCCCAACAAG 238
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 373 -----SerGlnProGlnProGlnProGln---ProGlnGln-ProProGlnGlnG 389
QY 239 CCCACATGTTCTTCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAGCAGCAGC 298
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 389 InProHisLeuValPro---ValSerLeuSerAsn---LeuLeu---ProGlySerProle 406
QY 299 GCATCTCTGGGCTTCAGTCTTT---CTCCAGAGCACAAAGGACTCTGGGTCTGACCTCA 355
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 406 uProHisValGlyAlaAlaLeuThrValThrHis-----ProHi 420
QY 356 CTGTTTCTGAGGACATCGGGGCTTAGAGTCTTAACACAGACTGTTTCCCTTCCAGCA 415
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 420 sIleSerIleLys-----SerGluProValSerProSerArgGl 433
QY 416 GAGAAAGAGTTCGAGAGCCACCCAGCC-----AAGCTGCAGCCCGGAGCTTACG 466
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 433 uArgSerProAlaProProProProAlaValPheProAlaAlaArgProGluProGlyGl 453
QY 467 AGGCTGGCTCCGCCCGGAGATGGAGTCAAGCAGAAAGGGCAGAGGATGAA 518
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 453 uGlyLeuSerSerProAlaGlyGlySerTyrGluThrGlyAspArgAsp 470
```

RESULT 15

A56201
transcription factor MEF2D isoform 1a - mouse
C:Species: Mus sp. (mouse)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 15-Mar-2004
C:Accession: A56201
R:Martin, J.F.; Milano, J.M.; Hustad, C.M.; Copeland, N.G.; Jenkins, N.A.; Olson, E.N.
Mol. Cell. Biol. 14, 1647-1656, 1994
A:Title: A Mef2 gene that generates a muscle-specific isoform via alternative mRNA splicing
A:Reference number: A56201; MUID:94158837; PMID:8114702
A:Accession: A56201
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-514 <MAR>
A:Cross-references: GB:S68893; NID:G545519; PIDN:AAB29973.1; PID:G545520
C:Genetics:
A:Gene: Mef2d
C:Keywords: alternative splicing; transcription factor
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

| | | | |
|------------------------|--------|---------------|-----|
| Pred. No.: | 1-62 | Length: | 514 |
| Score: | 96.50 | Matches: | 48 |
| Percent Similarity: | 44.38% | Conservative: | 23 |
| Best Local Similarity: | 30.00% | Mismatches: | 52 |
| Query Match: | 9.37% | Indels: | 37 |
| DB: | 2 | Gaps: | 10 |

US-10-659-782A-11 (1-579) x A56201 (1-514)

```
QY 62 ACCACTCCGCCAGGACTGCAG---GCCACCTGTCTGCAACCCAGCTGAGGCGCATGCCCT 118
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 351 SerSerProAlaGlyLeuAlaLeuGlyAsnValThrAlaTrpGln---GlnProGlnPro 369
QY 119 CCCAGGACCGTCTGTCAGCCCTCTGCTCCCTGGCATGCTCTGGCTGGAGATTGGCCATGG 178
```

```
Db 370 ProGlnProGln-ProProGlnProProGln----- 380
QY 179 CAGGCTCCAGCTTCTTCAGCCCTGAAACACAGAGAGTCCAGGTGAGACCTCCCAACAAG 238
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 381 -----SerGlnProGlnProProGlnProGln---ProGlnGln-ProProGlnGlnG 397
QY 239 CCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAGCAGCAGC 298
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 397 InProHisLeuValPro---ValSerLeuSerAsn---LeuLeu---ProGlySerProle 414
QY 299 GCATCTCTGGGCTTCAGTCTTT---CTCCAGAGCACAAAGGACTCTGGGTCTGACCTCA 355
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 414 uProHisValGlyAlaAlaLeuThrValThrHis-----ProHi 428
QY 356 CTGTTTCTGAGGACATCGGGGCTTAGAGTCTTAACACAGACTGTTTCCCTTCCAGCA 415
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 428 sIleSerIleLys-----SerGluProValSerProSerArgGl 441
QY 416 GAGAAAGAGTTCGAGAGCCACCCAGCC-----AAGCTGCAGCCCGGAGCTTACG 466
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 441 uArgSerProAlaProProProProAlaValPheProAlaAlaArgProGluProGlyGl 461
QY 467 AGGCTGGCTCCGCCCGGAGATGGAGTCAAGCAGAAAGGGCAGAGGATGAA 518
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 461 uGlyLeuSerSerProAlaGlyGlySerTyrGluThrGlyAspArgAsp 478
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Search completed: February 1, 2005, 13:29:29
Job time : 39 secs

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